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Abstracts

Pattern Formation in Development

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A systems biology approach to root development

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Central processes in development include creating distinctions between cells and producing coordination among different cells so that they function as units. In plants, both processes have been shown to rely heavily on cell-to-cell communication and activation and/or repression of subsets of genes. While signaling and transcription are equally important for development, high through-put techniques for identifying the nodes and links in transcriptional networks have matured more rapidly. For plants, the simplifying aspects of development in an organ such as the root make it highly tractable for the application of these approaches. The *Arabidopsis* root develops continuously from four sets of stem cells in its tip. Each stage of development is found in a specific set of cells along the longitudinal axis, with the youngest cells in each file being closest to the stem cells. The other simplifying aspect of root development is that it can be viewed as a radially symmetric cylinder. To identify the transcriptional networks that regulate plant development, three datasets are needed: (1) global expression profiles; (2) cellular localization of transcription factors; and (3) transcription factor targets. To understand the role of transcriptional networks in development, each of these datasets needs to be at cell-type-specific resolution. Methods for acquiring these types of data will be discussed, and results from many of the cell types in the root will be presented. Preliminary results on the effects of perturbing the networks with environmental stimuli will also be described.

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Patterning vertebrate head development

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The vertebrate hindbrain is patterned by a process of segmentation whereby a series of transient, lineage-restricted cellular compartments serve to establish regional diversity. This segmental organization impacts directly on craniofacial development by influencing the migration and character of neural crest cells. Environmental signals play key roles in the migration of cranial neural crest cells from the hindbrain rhombomeres into the branchial arches. We have investigated interactions that govern cranial neural crest cell migration and find that components of the Slit and Robo signaling pathway are involved in the migration and restriction of cells during head development. Blocking Robo or Slit1 activity results in a failure of migration of crest cells from the neural tube and an abnormal pattern of migration to cells already within the branchial arches. To further investigate interactions between the neural tube and surrounding tissues, we performed a functional screen and isolated a novel secreted molecule, WISE. Wise encodes a highly conserved secreted cystein-knot protein, which bears homology to known DAN, CCN and Slit family members. Analyses reveal that WISE is capable of activating and inhibiting Wnt signaling in a context-dependent manner, and this modulation depends upon components of the canonical Wnt pathway. Wise mutants display craniofacial, bone and eye defects. Our genetic studies indicate that Wise is part of a novel family of proteins with the dual potential to modulate the Wnt and BMP pathways in head development and patterning.

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A gene regulatory network for cell-type patterning in the *Arabidopsis* root epidermis

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Multicellular organisms possess diverse cell types that are organized in particular patterns. We seek to understand how cells acquire their distinct identities and form appropriate patterns within tissues. The root epidermis in *Arabidopsis* is useful for this purpose because it contains only two cell types (hair cells and non-hair cells) and mutations eliminating either cell type do not affect plant viability. Furthermore, the two cell

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